## In the Specification:

Please amend the specification as shown:

Please delete the paragraph on page 39, line 20 to line 27 and replace it with the following paragraph:

Purified HPV-16 E7 (lane1) (SEQ ID NO: 2) and HPV-18 E7 (lane2) (SEQ ID NO: 4) protein that was used for immunizations. The material was sequenced by Eurosequence B.V. (Netherlands); for results see example 2.3 and 5. 3 'Characterization of antigens used for immunization'. Proteins (5µg per lane) were separated in 12.5% SDS-PAGE under reducing conditions. HPV-18 E7 shows two characteristic bands due to N-terminal degradation as confirmed by sequencing (a sub-fraction of the protein starts with a Histidine (position14).

Please delete the paragraph on page 47, line 12 to line 27 and replace it with the following paragraph:

As confirmed by N-terminal sequencing, the main sequence is 100% in agreement with the expected N-terminal sequence of the E7 protein of human papilloma virus type 16. The main sequence was: (Met)-(His)-(Gly)-(Asp)-(Thr)-(Pro)-(Thr)-(Leu) (SEQ ID NO: 5). One of the minor signals at each position was brought into agreement with the n-2 mer of the protein: (Gly)-(Asp)-(Thr)-(Pro)-(Thr)-(Leu)-(His)-(Glu) (SEQ ID NO: 6); this was approx. 20% with regard to the main sequence. The remaining minor signals were brought into agreement with the n-1 mer of the protein: (His)-(Gly)-(Asp)-(Thr)-(Pro)-(Thr)-(Leu)-(His) (SEQ ID NO: 7); this was approx. 7% with regard to the main sequence. To conclude, 73% of the sample are full length HPV16-E7, 7% are degraded at the N-terminus missing one amino acid (Met) and 20% are degraded at the N-terminus missing two amino acids (Met, His).

Sequencing yield and result was:

position: 1 5
83% (SEQ ID NO: 5) (Met)-(His)-(Gly)-(Asp)-(Thr)-(Pro)-(Thr)-(Leu)-

Please delete the paragraph on page 49, line 14 to line 20 and replace it with the following paragraph:

The interpretation of the obtained fragments on the basis of known sequence information allows the following conclusion.

fragment 1 (N-terminus):	(SEQ ID NO: 8) (Met)-(His)-(Gly)-(Asp)-(Thr)-
(Pro)	
fragment 2 (cleaved at AA 49):	(SEQ ID NO: 9)(Ala)-(His)-(Tyr)-(Asn)-(Ile)-
(Val)	
fragment 3 (cleaved at AA 60):	(SEQ ID NO: 10) (Cys)-(Asp)-(Ser)-(Thr)-(Leu)-
(Arg)	
fragment 4 (cleaved at AA 66):	(SEQ ID NO: 11) (Leu)-(Cys)-(Val)-(Gln)-(Ser)-
(Thr)	
fragment 5 (cleaved at AA 77):	(SEQ ID NO: 12) (Thr)-(Leu)-(Glu)-(Asp)-(Leu)-
(Leu)	

Please delete the paragraph on page 84, line 28 to page 85, line 16 and replace it with the following paragraph:

As confirmed by N-terminal sequencing, the main sequence is 100% in agreement with the expected N-terminal sequence of the E7 protein of human papilloma virus type 18. The main sequence was: (Met)-(His)-(Gly)-(Pro)-(Lys)-(Ala)-(Thr)-(Leu) (SEQ ID NO: 13). One of the minor signals at each position was brought into agreement with the n-1 mer of the protein: (His)-(Gly)-(Pro)-(Lys)-(Ala)-(Thr)-(Leu)-(Gln) (SEQ ID NO: 14); this was approx. 16 - 20% with regard to the main sequence. The remaining minor signals were brought into agreement with the n-12 mer of the protein: (His)-(Leu)-(Glu)-(Pro)-(Gln)-(Asn)-(Glu)-(Ile) (SEQ ID NO: 15); this again was approx. 16 - 20% with regard to the main sequence. To conclude, 60 - 68% of the sample are full length HPV18-E7, 16 - 20% are degraded at the N-terminus missing one amino acid (Met) and 16 - 20% are degraded at the N-terminus missing 13 amino acids (Met, His, Gly, Asp, Thr, Pro, Thr, Leu, Gln, Asp, Ile, Val, Leu). The

truncated protein has a calculated WM of 10.6 kDa compared to 12.0 kDa of the full length protein. The difference in size is also seen in SDS-PAGE, Fig.3.

Sequencing yield and result was:

position:	1	5	
60 - 68%	(SEQ ID NO: 13)(Met)-(His)-(Gly	r)-(Pro)-(Lys)-(Ala)-(Thr)-(L	eu)-
16 – 20%	(SEQ ID NO: 14) (His)-(Gly)	-(Pro)-(Lys)-(Ala)-(Thr)-(Le	u)-(Gln)
position:	15	20	
16 - 20% <b>(S</b>	EQ ID NO: 15) (His)-(Leu)-(Glu)-(P	ro)-(Gln)-(Asn)-(Glu)-(Ile)	

Please delete the paragraph on page 87, line 15 to line 24 and replace it with the following paragraph:

The interpretation of the obtained fragments on the basis of known sequence information allows the following conclusion: (\* minor sequences)

fragment 1 (N-terminus): (SEQ ID NO: 16)(Met)-(His)-(Gly)-(Pro)-(Lys)
fragment 2 (cleaved at AA 5): (SEQ ID NO: 17)(Ala)-(Thr)-(Leu)-(Gln)-(Asp)-(Ile)
fragment 3* (N-terminus truncated): (SEQ ID NO: 18)(His)-(Leu)-(Glu)-(Pro)-(Gln)-
(Asn)
fragment 4 (cleaved at AA 52): (SEQ ID NO: 19)(Arg)-(Ala)-(Glu)-(Pro)-(Gln)-(Arg)
fragment 5 (cleaved at AA 53): (SEQ ID NO: 20)(Ala)-(Glu)-(Pro)-(Gln)-(Arg)-(His)
fragment 6* (cleaved at AA 58): (SEQ ID NO: 21)(His)-(Thr)-(Met)-(Leu)-(Cys)-(Met)
fragment 7* (cleaved at AA 67): (SEQ ID NO: 22)(Cys)-(Glu)-(Ala)-(Arg)-(Ile)-(Glu)
fragment 8* (cleaved at AA 71): (SEQ ID NO: 23) (Ala)-(Phe)-(Gln)-(Gln)-(Leu)-
(Phe)